

1 / 12

FIGURE 1

Figure 1 continued

3/12

Lc743	N	C	A	N	F	G	G	N	P	D	N	I	T	V	F	G	E	S	A	G	220
RM8con
601	660
Lc743	AATTGCGCCAACCTTGGTGGCAATCCCGATAATATTACAGTCTTGGTAAAGTGCCGGT																				
RM8A																				
RM8B																				
RM8C																				
RM8con																				
 Lc743	A	A	S	T	H	Y	M	M	L	T	E	Q	T	R	G	L	F	H	R	G	240
RM8con
661	720
Lc743	GCTGCCTCTACCCACTACATGATGTTAACCGAACAAACTCGGGTCTTTCCATCGTGGT																				
RM8A																				
RM8B																				
RM8C																				
RM8con																				
 Lc743	I	L	M	S	G	N	A	I	C	P	W	A	N	T	Q	C	Q	H	R	A	260
RM8con	L
721	780
Lc743	ATACTAATGTCGGGTAATGCTATTTGTCCATGGGCTAATACCCAAATGTCAACATCGTGGC																				
RM8AT.....																				
RM8BT.....																				
RM8CT.....																				
RM8conT.....																				
 Lc743	F	T	L	A	K	L	A	G	Y	K	G	E	D	N	D	K	D	V	L	E	280
RM8con	L
781	840
Lc743	TTCACCTTAGCCAAATTGGCCGGCTATAAGGGTGAGGATAATGATAAGGATTTGGAA																				
RM8A																				
RM8B																				
RM8CA.....																				
RM8con																				
 Lc743	F	L	M	K	A	K	P	Q	D	L	I	K	L	E	E	K	V	L	T	L	300
RM8con
841	900
Lc743	TTTCTTATGAAAGCCAAGCCACAGGATTAAATAAAACTTGAGGAAAAAGTTTAACCTCA																				
RM8A																				
RM8B																				
RM8CG.....																				
RM8con																				

Figure 1 continued

Lc743	E	E	R	T	N	K	V	M	F	P	F	G	P	T	V	E	P	Y	Q	T	320
RM8con
901	960
Lc743	GAAGAGCGTACAAATAAGGTATGTTCCCTTGGTCCCAGTGTGAGCCATATCAGACC																				
RM8A																				
RM8B																				
RM8C																				
RM8con																				
Lc743	A	D	C	V	L	P	K	H	P	R	E	M	V	K	T	A	W	G	N	S	340
RM8con
961	1020
Lc743	GCTGATTGTGTCTTACCCAAACATCCTCGGGAAATGGTTAAACTGCTTGGGTAATTG																				
RM8A																				
RM8B																				
RM8C																				
RM8con																				
Lc743	I	P	T	M	M	G	N	T	S	Y	E	G	L	F	F	T	S	I	L	K	360
RM8con
1021	1080
Lc743	ATACCCACTATGATGGGTAACACTTCATATGAGGGCTATTTTCAATTCTTAAG																				
RM8A																				
RM8B																				
RM8C																				
RM8con																				
Lc743	Q	M	P	M	L	V	K	E	L	E	T	C	V	N	F	V	P	S	E	L	380
RM8con
1081	1140
Lc743	CAAATGCCTATGCTTGTAAAGGAATTGGAAACTTGTGTCAATTGTGCCAAGTGAATTG																				
RM8A																				
RM8B																				
RM8C																				
RM8con																				
Lc743	A	D	A	E	R	T	A	P	E	T	L	E	M	G	A	K	I	K	K	A	400
RM8con
1141	1200
Lc743	GCTGATGCTGAACGCACCGCCCCAGAGACCTTGGAAATGGGTGCTAAAATAAAAAGGCT																				
RM8AT.....																				
RM8B																				
RM8C																				
RM8con																				

Figure 1 continued

5/12

Lc743	H	V	T	G	E	T	P	T	A	D	N	F	M	D	L	C	S	H	I	Y	420
RM8con
1201	+1260
Lc743	CATGTTACAGGAGAACACCAACAGCTGATAATTTATGGATCTTGCTCACATCTAT																				
RM8A	
RM8B	
RM8C	
RM8con	
 Lc743	F	W	F	P	M	H	R	L	L	Q	L	R	F	N	H	T	S	G	T	P	440
RM8con	
1261	+1320
Lc743	TTCTGGTTCCCCATGCATCGTTGTTGCAATTACGTTCAATCACACCTCCGGTACACCC																				
RM8A		
RM8B		
RM8C		
RM8con		
 Lc743	V	Y	L	Y	R	F	D	F	D	S	E	D	L	I	N	P	Y	R	I	M	460
RM8con	
1321	+1380
Lc743	GTCTACTTGTATCGCTTCGACTTGTGATTCTGGAAAGATCTTATTAAATCCCTATCGTATTATG																				
RM8A	C	C	
RM8B	C	C	
RM8C	C	C	
RM8con	C	C	
 Lc743	R	S	G	R	G	V	K	G	V	S	H	A	D	E	L	T	Y	F	F	W	480
RM8con	
1381	+1440
Lc743	CGTAGTGGACGTGGTGTAAAGGGTGTAGTCATGCTGATGAATTACCTATTCTCTGG																				
RM8A		
RM8B		
RM8C		
RM8con		
 Lc743	N	Q	L	A	K	R	M	P	K	E	S	R	E	Y	K	T	I	E	R	M	500
RM8con	
1441	+1500
Lc743	AATCAATTGGCCAAACGTATGCCCTAAAGAACCGCTGAATACAAAACAATTGAACGTATG																				
RM8A		
RM8B		
RM8C		
RM8con		

Figure 1 continued

SUBSTITUTE SHEET (RULE 26)

6/12

Lc743	T	G	I	W	I	Q	F	A	T	T	G	N	P	Y	S	N	E	I	E	G	520
RM8con
1501	-----+1560																				
Lc743	ACTGGTATATGGATACAATTGCCACCACTGGTAATCCTTATAGCAATGAAATTGAAGGT																				
RM8A	
RM8B	
RM8C	
RM8con	
 Lc743	M	E	N	V	S	W	D	P	I	K	K	S	D	E	V	Y	K	C	L	N	540
RM8con	
1561	-----+1620																				
Lc743	ATGGAAAATGTTCTGGGATCCAATTAAGAAATCCGACGAAGTATAAGTGTGTTGAAT																				
RM8A	
RM8B	
RM8C	
RM8con	
 Lc743	I	S	D	E	L	K	M	I	D	V	P	E	M	D	K	I	K	Q	W	E	560
RM8con	
1621	-----+1680																				
Lc743	ATTAGTGACGAATTGAAAATGATTGATGTGCCTGAAATGGATAAGATTAAACAATGGAA																				
RM8A	T	G	
RM8B	T	G	
RM8C	T	G	
RM8con	T	G	
 Lc743	S	M	F	E	K	H	R	D	L	F	*	570									
RM8con	
1681	-----+1713																				
Lc743	TCGATGTTGAAAAACATAGAGATTATTTAG																				
RM8A	
RM8B	
RM8C	
RM8con	

Figure 1 continued

7/12

Figure 2.

Md α E7 1 MTFLKQFIFRLKLCVKCMVNKYTNYRLSTNETQIIDTEYGQIKGVKRMTV 50
 | . | : : || : : || : || | . || | : : || | . : || | : || | : ||
 Lc α E7 1 MNFNVSLMEKLWKIKCIENKFLNYRLTTNETVVAETEYGVKGVKRMTV 50

51 YDDSYYSFESIPYAKPPVGEFLRFKAPQRPVWEGVRDCCGPANRSVQTDF 100
 || | | | | : || | . || | | | | | | | . || : || | . . : || | . ||
 51 YDDSYYSFEGIPYAQPPVGEFLRFKAPQRPTPWDGVRDCCNHKDKSVQVDF 100

101 ISGKPTGSEDCLYLNVYTNDLNPDKRRPVMVFIHGGDFIFGEANRNWFGP 150
 | . | | . | | | | . | | | : | | | : | | | : | | | : | | . : | |
 101 ITGKVCVGSEDCLYLSVYTNNLNPETKRPVLVYIHGGFIIGENHRDMDYGP 150

151 DYFMKKPVVLVTQYRLGVLGFLSLKSENLNVPGNAGLKDVQVMAWRWVKS 200
 | | | : | | | : | | | | . | | : | | | | | | | | | | | | | : | .
 151 DYFIKKDVVLINIQYRLGFLSLNSEDLNVPGNAGLKDVQVMAWRWIKN 200

201 NIAIFGGDVNDNITVFGESAGGASTHYMMITEQTRGLFHRGIMMSGNSMCS 250
 | . | | | : | | | | : | | | | : | | | | | | | | | | | | : | .
 201 NCANFGGNPDNITVFGESAGAASTHYMMITEQTRGLFHRGILMSGNAICP 250

251 WASTECQSRALTMAKRVGYKGEDNEKDILEFLMKANPYDLIKEPQLTP 300
 | . | : | | | : | | . | | | | | : | | | | | | | | | | | | | . | |
 251 WANTQCQHRAFTLAFLAGYKGEDNDKDVLEFLMKAKPQDLIKEEKVTL 300

301 ERMQNKMFPFGPTVEPYQTADCVVPKPIREMVKSAWGNISIPTLIGHTSY 350
 | . | | | | | | | | | | | | : | . | | | | | | | | | | | | : | | |
 301 EERTNKVMFPFGPTVEPYQTADCVLPHPREMVKTAWGNISIPTMMGNTSY 350

351 EGLLSKSVAKQYYPEVVKELESCVNYVPWEADSERSAPETLERAIVKKA 400
 | | | : . | | | : | | | | . | | | | | | | | | | | | | | | | : | | |
 351 EGLFFTSILKQMPMLVKELETCVNFVPSLADAERTAPETLEMGAKIKKA 400

401 HVGETPTLDNFMLECSYFYFLFPMPHRLQLRFNHTAGTPYLYRFDfds 450
 | | | | | | | : | | | : | | | | : | | | | | | | | | | | | | | | | |
 401 HVTGETPTADNFMDLCSHIYFWFPMPHRLQLRFNHTSGTPVYLYRFDfds 450

451 EEEINPYRIMRGRGVKGVSHADELTYLFWNILSKRLPKESREYKTIERM 500
 | : | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
 451 EDLINPYRIMRSRGVKGVSHADELTYFFWNQLAKRMPKESREYKTIERM 500

501 VGIWTEFATTGKPYNSNDIAGMENLTWDPPIKKSDDVYKCLNIGDELKVML 550
 | | | : | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
 501 TGIWIQFATTGNPYSNEIEGMENVSWDPIKKSDEVYKCLNISDELKMDV 550

551 PEMDKIKQGASIFDKKKELF 570
 | | | | | | . | : | : | . : | |
 551 PEMDKIKQWESMFKEHRDLF 570

8/12

Figure 3.

ATGACTTTCTGAAGCAATTCAATTGCGCTGAAACTATGCTTAAATGCATGGTCAAT
 1 -----+-----+-----+-----+-----+-----+ 60
 TACTGAAAAGACTTCGTTAAGTATAAACGGACTTGTACGAAATTACGTACCAAGTTA

 M T F L K Q F I F R L K L C F K C M V N -

 AAATACACAAACTACCGTCTGAGTACAAATGAAACCCAAATAATCGATACTGAATATGGA
 61 -----+-----+-----+-----+-----+-----+ 120
 TTTATGTGTTGATGGCAGACTCATGTTACTTGGGTTATTAGCTATGACTTACCT

 K Y T N Y R L S T N E T Q I I D T E Y G -

 CAAATTAAGGGTGTAAAGCGAATGACCGTCTACGATGATTCTACTACAGTTGAGAGT
 121 -----+-----+-----+-----+-----+-----+ 180
 GTTTAATTCCCACAATTGCTTACTGGCAGATGCTACTAAGAATGATGTCAAAGCTCTCA

 Q I K G V K R M T V Y D D S Y Y S F E S -

 ATACCCTATGCTAACGCCTCCAGTGGGTGAGTTGAGATTCAAGGCACCCCAGCGGCCTGTA
 181 -----+-----+-----+-----+-----+-----+ 240
 TATGGGATACGATTGGAGGTACCCACTCAACTCTAACGTTCCGTGGGTCGCCGGACAT

 I P Y A K P P V G E L R F K A P Q R P V -

 CCATGGGAGGGTGTACGTGATTGCTGTGGGCCAGCCAACAGATCGGTACAGACAGATTTC
 241 -----+-----+-----+-----+-----+-----+ 300
 GGTACCCCTCCCACATGCACTAACGACACCCGGTCGGTTGTCTAGCCATGTCTAAAG

 P W E G V R D C C G P A N R S V Q T D F -

 ATAAGTGGCAAACCCACAGGTTGGAGGATTGTCTACCTGAATGTGTACCAATGAC
 301 -----+-----+-----+-----+-----+-----+ 360
 TATTACCGTTGGGTGTCCAAGCCTCTAACAGATATGGACTACACATATGGTTACTG

 I S G K P T G S E D C L Y L N V Y T N D -

 TTGAACCCAGACAAAAGCGTCTGTTATGGTTTCATCCATGGCGGAGATTTATTTTC
 361 -----+-----+-----+-----+-----+-----+ 420
 AACTTGGGTCTGTTTCCGCAGGACAATACCAAAAGTAGGTACCGCCTCTAAAATAAAAG

 L N P D K R R P V M V F I H G G D F I F -

 GGCGAAGCAAATCGTAACTGGTTGGTCCCAGTACTTATGAAGAAACCCGTGGCTTG
 421 -----+-----+-----+-----+-----+-----+ 480
 CCGCTTCGTTAGCATTGACCAAACCAAGGGCTGATGAAATACTTCTTGGGCACCAAC

 G E A N R N W F G P D Y F M K K P V V L -

9/12

481 GTAACCGTGCAATATCGTTGGGTGTGGGTTCCCTAGCCTGAAATCGGAAAATCTC
 540 CATTGGCACGTTATAGCAAACCCACACAACCCAAAGGAATCGGACTTAGCCTTTAGAG
 541 V T V Q Y R L G V L G F L S L K S E N L -
 541 AATGTCCCCGGCAACGCTGGCCTCAAGGATCAAGTAATGGCCTTGAGATGGGTCAAGAGT
 600 TTACAGGGGCCGTTGCGACCGGAGTTCTAGTTCACTACCGGAACTCTACCCAGTTCTCA
 601 N V P G N A G L K D Q V M A L R W V K S -
 601 AATATTGCCATTTCGGTGGCGATGTAGACAATATTACCGTCTCGGCAGAAAGTGCTGGT
 660 TTATAACGGTAAAAGCCACCGCTACATCTGTTATAATGGCAGAAGCCGTTCACGACCA
 661 N I A I F G G D V D N I T V F G E S A G -
 661 GGGGCCTCAACCCATTACATGATGATAACCGAACAGACCCGTGGTTATTCCATCGTGGT
 720 CCCCCGAGTTGGTAATGTACTACTATTGGCTGTGGCACCAAATAAGGTAGCACCA
 721 G A S T H Y M M I T E Q T R G L F H R G -
 721 ATCATGATGTCCGGTAATTCCATGTGCTCATGGCCTCTACAGAACGAAAGTCGTGCG
 780 TAGTACTACAGGCCATTAAGGTACACGAGTACCCGGAGATGTCTACGGTTACGCACGC
 781 I M M S G N S M C S W A S T E C Q S R A -
 781 CTCACCATGGCAAACGTGTTGGCTATAAGGGAGAGGACAATGAAAAAGATATCCTGGAA
 840 GAGTGGTACCGGTTGCACAACCGATATTCCCTCTCCTGTACTTTCTATAGGACCTT
 841 L T M A K R V G Y K G E D N E K D I L E -
 841 TTCCTAATGAAAGCCAATCCCTATGATTGATCAAAGAGGGAGCCACAAGTTTGACACCC
 900 AAGGATTACTTCGGTTAGGGATACTAAACTAGTTCTCCTCGGTGTTCAAAACTGTGGG
 901 F L M K A N P Y D L I K E E P Q V L T P -
 901 GAAAGAATGCAAATAAGGTCAATGTTCTTTGGACCCACTGTAGAACCATACCAAGACA
 960 CTTTCTTACGTTTATTCCAGTACAAAGGAAACCTGGGTGACATCTGGTATGGCTGT
 961 E R M Q N K V M F P F G P T V E P Y Q T -
 961 GCCGACTGTGTTACCCAAACCAATCAGAGAAATGGTGAAGAGGCCCTGGGAAATTGCG
 1020 CGGCTGACACACCATGGGTTGGTAGTCTCTTACCACTCTCGCGAACCCCTTAAGC
 1020 A D C V V P K P I R E M V K S A W G N S -

Figure 3 continued

SUBSTITUTE SHEET (RULE 26)

10/12

1021 ATACCCACATTGATAGGCAATACCTCCTACGAAGGTTGCTTCAAATCAATTGCCAA 1080
 TATGGGTGTAACTATCCGTTATGGAGGATGCTTCAAACGAAAGGTTAGTTAACGGTT
 I P T L I G N T S Y E G L L S K S I A K -
 CAATATCCGGAGGTTGTAAGAGTTGGAATCCTGTGTGAATTATGTGCCCTGGGAGTTG 1140
 1081 GTTATAGGCCTCCAACATTTCTCAACCTAGGACACACTTAATACACGGAAACCTAAC
 Q Y P E V V K E L E S C V N Y V P W E L -
 GCTGACAGTGAACGCAGTGCCCCGGAAACCCCTGGAGAGGGCTGCCATTGTGAAAAAGGCC 1200
 1141 CGACTGTCACTTGCGTCACGGGCCTTGGACCTCTCCGACGGTAACACTTTCCGG
 A D S E R S A P E T L E R A A I V K K A -
 CATGTGGATGGGAAACACCTACTCTGGATAATTATGGAGCTTGCTCTATTCTAT 1260
 1201 GTACACCTACCCCTTGTGGATGAGACCTATTAAAATACCTCGAAACGAGGATAAAGATA
 H V D G E T P T L D N F M E L C S Y F Y -
 TTCCCTTCCCCATGCATCGCTTACAATTGCGCTCAACCACACAGCTGGCACTCCC 1320
 1261 AAGGAGAAGGGTACGTAGCGAAGGATGTTAACCGCAAGTTGGTGTGACCGTGAGGG
 F L F P M H R F L Q L R F N H T A G T P -
 ATTTATTTGTATCGTTGATTGATTCCGAAGAAATTATTAACCCCTATCGTATTATG 1380
 1321 TAAATAAACATAGCAAAGCTAAAGCTAAGGCTTAAATAATTGGGATAGCATAATAC
 I Y L Y R F D F D S E E I I N P Y R I M -
 CGTTTGGCCGTGGCGTTAAAGGTGTAAGCCATGCCGATGAGCTAACCTATCTCTGG 1440
 1381 GCAAAACCGGCACCGCAATTCCACATTCGGTACGGCTACTCGATTGGATAGAGAACCC
 R F G R G V K G V S H A D E L T Y L F W -
 AACATTTGTCGAAACGCCTGCCAAAGGAAAGCCCGAATACAAACATTGAACGCATG 1500
 1441 TTGTAAAACAGCTTGGACGGTTCTTCGGCGTTATGTTGGTAACCTGCGTAC
 N I L S K R L P K E S R E Y K T I E R M -
 GTTGGCATTGGACGGAATTGCCACCAACGGCAAACCATACAGCAATGATAGCCGGC 1560
 1501 CAACCGTAAACCTGCCTTAACCGGTGGTGGCCGTTGGTATGCGTTACTATACGGCCG
 V G I W T E F A T T G K P Y S N D I A G -

Figure 3 continued

11/12

ATGGAAAACCTCACCTGGGATCCCATAAAAAAATCCGATGATGTCTATAAATGTTAAAT
1561 -----+-----+-----+-----+-----+-----+ 1620
TACCTTTGGAGTGGACCCTAGGGTATTTTTAGGCTACTACAGATATTACAAATTAA

M E N L T W D P I K K S D D D V Y K C L N -

ATCGGCGATGAATTGAAAGTTATGGATTGCCAGAAATGGATAAAATTAAACAATGGGCA
1621 -----+-----+-----+-----+-----+-----+ 1680
TAGCCGCTACTTAACCTTCAATACCTAAACGGTCTTACCTATTTAATTGTTACCCGT

I G D E L K V M D L P E M D K I K Q W A -

AGTATATTGATAAAAAGAAGGAATTGTTT
1681 -----+-----+-----+ 1710
TCATATAAGCTATTTCTTCCTTAACAAA

S I F D K K K E L F

Figure 3 continued

Figure 4..

MdaE7 97 QTDFISGKPTGSEDCLYLNVYTNDLNPDKKRPMVFIHGGGFIFGEANRN 146
 |.|||.|.|||.|.|||:|||:|||:|||:|||:|||:|||:|||:|||:
 LcαE7 97 QVDFITGKVCVGSEDCLYLSVYTNNLNPETKRPVLVYIHGGGFIIGENHRD 146
 . . .
 147 WYGPDYFMKKPVVLTVQYRLGVLGFLSLKSENLNVPGNAGLKDVQVIMALR 196
 |||||:|||.|||:|||:|||:|||:|||:
 147 MYGPDYFIKKDVVLINIQYRLGALGFLSLSNEDLNVPGNAGLKDVQVIMALR 196
 . . .
 197 WFKSNIAIFGGDVNDNITVFGESAGGASTHYMMITEQTRGLFHRCIMMSGN 246
 |:|.|||:|||:|||:|||:|||:|||:|||:|||:|||:
 197 WIKNNCANFGGNDNITVFGESAGAASTHYMMLTEQTRGLFHRCILMSGN 246
 ↓ . . .
 247 SMCSSASTECQSRALTMAKRVGYKGEENEKDILEFLMKANPYDLIKEEPQ 296
 .|||.|||:|||:|||:|||:|||:|||:|||:|||:|||:
 247 AICPLANTQCQHRAFTLAKLAGYKGEDNDKDVLFLMKAKPQDLIKLEEK 296
 . . .
 297 VLTPERM 303
 ||| | .
 297 VLTLEER 303